

Figure 1A: DNA sequence of the murine *edg-5* RT-PCR clone 501 (SEQ ID NO: 3)

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1   AACACTGGCG CGGTGTCGAA AACGTTGACC GTCAAACGCT GGTTCCTCCG
51  CCAGGGGCTC CTAGACACCA GCCTGACTGC CTCCCTGGCC AATTTGCTGG
101 TTATTGCTGT GGAAAGACAC ATGTCNATCA TGAGGATGAG AGTCCACAGC
151 AACTTGACCA AAAAGCGGGT GACGCTGCTC ATTCTGCTGG TGTGGGGCCAT
201 CGCCATCTTC ATGGGGGGCCG TCCCCACNCT GGGATGGAAT TGCCTCTGCA
251 ACATCTCGGC CTGCTCTTCT CTGGCTCCCA TTTACAGTAG GAGTTACCTC
301 ATTTTCTGGA CTGTGTCCAA CCTCCTGGCC TTCTTCATCA TGGTGGCGGT
351 ATACGTACGC ATCTACATGT ATGTTAAAAG GAAAACCAAC GTCTTATCTC
401 CACACACCAG TGGCTCCATC AGCCGCCGGA GGGCTCCCAT GAAGCTAATG
451 AAGACAGTGA TGACCGTCTT AGGCGCCTTC GTGGTGTGCT GGACCCCGGG
501 TCTGGTGGTT CTGCTGCTGG ACGGCCTGAA CTGCAAGCAG TGTAACGTGC
551 AACACGTGAA GNGCTGGTTC CTGCTGCTCG CACTGCTCAA CTCCGTCATG
601 AACCCCTCA TCTACTGCCG CTCTCCNNAC TTTCCATGG

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Figure 1B: Sequence of full-length *mEDG-5* cDNA insert and alignment with *MEDG-5* amino acid sequence. Translation starts at nt 19. Translation termination codon is located at nt 1081-1083

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                                M N E C H Y D K R M D F F Y
1   GCACAGTTCTTGTCCACCATGAATGAGTGTCACTATGACAAGCGCATGGACTTTTCTAC
-----+-----+-----+-----+-----+-----+-----+ 60

N R S N T D T A D E W T G T K L V I V L
61  AACAGGAGCAACACAGACACAGCGGACGAGTGGACAGGGACAAAGCTTGTGATCGTCCTG
-----+-----+-----+-----+-----+-----+ 120

C V G T F F C L F I F F S N S L V I A A
121 TGCGTGGGGACGTTCTTCTGCCTCTTTATATTTTTTCTAACTCCCTGGTCATTGCTGCG
-----+-----+-----+-----+-----+-----+ 180

V I T N R K F H F P F Y Y L L A N L A A
181 GTGATCACAACCGGAAGTTCCACTTTCCCTTCTACTACCTGCTGGCTAACTTAGCTGCT
-----+-----+-----+-----+-----+-----+ 240

A D F F A G I A Y V F L M F N T G P V S
241 GCGGATTTCTTCGCCGAATCGCTTACGTGTTCTGATGTTTAACTGGCCCGGTGTCG
-----+-----+-----+-----+-----+-----+ 300

K T L T V N R W F L R Q G L L D T S L T
301 AAAACGTTGACCGTCAACCGCTGGTTCCTCCGCCAGGGGCTCCTAGACACCAGCCTGACT
-----+-----+-----+-----+-----+-----+ 360

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Figure 1B (cont.)

	A S L A N L L V I A V E R H M S I M R M	
	GCCTCCCTGGCCAATTTGCTGGTTATTGCTGTGGAAAGACACATGTCAATCATGAGGATG	
361	-----+-----+-----+-----+-----+-----+	420
	R V H S N L T K K R V T L L I L L V W A	
	AGAGTCCACAGCAACTTGACCAAAAAGCGGGTGACGCTGCTCATTCTGCTGGTGTGGGCC	
421	-----+-----+-----+-----+-----+-----+	480
	I A I F M G A V P T L G W N C L C N I S	
	ATCGCCATCTTCATGGGGGCGTCCCCACGCTGGGATGGAATTGCCTCTGCAACATCTCG	
481	-----+-----+-----+-----+-----+-----+	540
	A C S S L A P I Y S R S Y L I F W T V S	
	GCCTGCTCTTCTCTGGCTCCCATTTACAGTAGGAGTTACCTCATTTTCTGGACTGTGTCC	
541	-----+-----+-----+-----+-----+-----+	600
	N L L A F F I M V A V Y V R I Y M Y V K	
	AACCTCCTGGCCTTCTTCATCATGGTGGCGGTATACGTACGCATCTACATGTATGTTAAA	
601	-----+-----+-----+-----+-----+-----+	660
	R K T N V L S P H T S G S I S R R R A P	
	AGGAAAACCAACGTCTTATCTCCACACACCAAGTGGCTCCATCAGCCGCCGGAGGGCTCCC	
661	-----+-----+-----+-----+-----+-----+	720
	M K L M K T V M T V L G A F V V C W T P	
	ATGAAGCTAATGAAGACAGTGATGACCGTCTTAGGCGCCTTCGTGGTGTGCTGGACCCCG	
721	-----+-----+-----+-----+-----+-----+	780
	G L V V L L L D G L N C K Q C N V Q H V	
	GGTCTGGTGGTTCTGCTGCTGGACGGCCTGAACTGCAAGCAGTGTAACGTGCAACACGTG	
781	-----+-----+-----+-----+-----+-----+	840
	K R W F L L L A L L N S V M N P I I Y S	
	AAGCGTGTTCTGCTGCTCGCACTGCTCAACTCCGTCATGAACCCCATCATCTACTCG	
841	-----+-----+-----+-----+-----+-----+	900
	Y K D E D M Y N T M R K M I C C A L Q D	
	TACAAGGACGAGGACATGTACAACACCATGCGGAAGATGATCTGCTGTGCCCTGCAGGAC	
901	-----+-----+-----+-----+-----+-----+	960
	S N T E R R P S R N P S T I H S R S E T	
	AGCAATACCGAGAGGCGCCCCCTCCCGCAACCCCTCCACCATCCACAGCAGGAGCGAGACG	
961	-----+-----+-----+-----+-----+-----+	1020
	G S Q Y L E D S I S Q G P V C N K N G S	
	GGCAGCCAGTACCTGGAGGACAGCATCAGCCAGGGCCCGGTGTGCAATAAAAACGGCTCC	
1021	-----+-----+-----+-----+-----+-----+	1080
	*	
	TAAGCCACGGACGCCTCCGCCCTCTTCCCCTGGGGAAAGAGCTGTTAAGCGTCTCTACCT	
1081	-----+-----+-----+-----+-----+-----+	1140
	GTCTCACAAAGCACGTGGACAGGGTTGTTTGAGGGCTCCATGCATCACTTCTGGGGCTTT	
1141	-----+-----+-----+-----+-----+-----+	1200

058125 150400

Figure 1B (cont.)

	TAAGTTTTCATGGTCAAGGAAAATAGATTTACGGCGTTTTAGTAAAGCGCACAGGAAAGGG	
1201	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1260
	AGAGATGAGCAGTGGGTTCCGGCTTGTCTGTGATCCGCTCCCAACATCCTCCAGCTCTTG	
1261	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1320
	CGAGAGCATGCTGGGCTCTGTCACCATCTTGCCACCATTGTCTGTGTGTTTTCAATGATG	
1321	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1380
	GTGTTGAAAGTCCTAGGTCAAAAGAAAGTAGTAAATAATGGTACCTGAGCCCCCATTGT	
1381	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1440
	GTGGCTACTAGATTCTGTAGTTGTTTCCGCATGGGTTTAAATGTTCAGAAAAATATTTT	
1441	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1500
	AGCAGTGAACTTTGATTTCTCTCAGAGAAGCCATGGCCAGGAGCTAGGTGGGCAACTGTAT	
1501	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1560
	AGTAGAGTAAGTGATGATATTGACCGGTAGGTTGAACTTCTTCAAATAGCGTCAAATAT	
1561	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1620
	GAGCACGATTAGATCTTCAGTCTTGGTTATCAGGATACCGCTGAGGGGCTTGCTGGATCC	
1621	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1680
	CAAGTGCAAAGTAATTGCACATCGAGTATTTTAACCAAAGCTGCCAGCGTATTCTATCTT	
1681	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1740
	GTGGACTGCATTTTGATCTTGATTTTTTCTCCTTCAAAGACCTCTGAAAGGTAGATCAGT	
1741	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1800
	TAAAAACA AAAAATAGTGTTTCATACACATAGGCTACTGACCAGTGTTTTCGGTGTAAGACG	
1801	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1860
	TTTAGAGTGTATCTGACAAAGTAAGAATAA CT TCAAGGCAGGCACTATGGTATTTATGTA	
1861	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1920
	GCTTGCAAACGTTTACATGTTCTCTCTCTCTCTCTCTCCCCTCTGCTGTTGTGATGTA	
1921	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	1980
	ACATTTATGTGCACAAACTACTTGTAATAAAATATTTTAAGAAGCAAAAAAAAAA	
1981	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	2033

Figure 2: Predicted amino acid sequence of Mouse partial EDG-5 cDNA. X represents an amino acid which cannot be assigned due to poor sequencing information from direct PCR sequencing

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1  NTGPGVSKTLT VNRWFLRQGL LDTSLTASLA NLLVIAVERH MSIMRMRVHS
51  NLTKKRVTL LLLVWVIAIF MGAVPTLGWN CLCNISACSS LAPIYSRSL
101 IFWTVSNLLA FFIMVAVYVR IYMYVKRKTN VLSPHTSGSI SRRRAPMKLM
151 KTVMTVLGAF VVCWTPGLVV LLLDGLNCKQ CNVQHVXWF LLLALLNSVM
201 NPLIYCRSPX FPW

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Figure 3A: Nucleotide sequence of a hEDG-5 cDNA inserted into pcDNA3 (SEQ ID NO:13)

Start and stop codons underlined.

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1  gaattcgcgg ccgcgtcgac gttcaCTTCT CCACAATGAA TGAGTGTCAC
51  TATGACAAGC ACATGGACTT TTTTATAAT AGGAGCAACA CTGATACTGT
101 CGATGACTGG ACAGGAACAA AGCTTGTGAT TGTTTTGTGT GTTGGGACGT
151 TTTTCTGCCT GTTTATTTTT TTTTCTAATT CTCTGGTCAT CGCGGCAGTG
201 ATCAAAAACA GAAAATTTCa TTTCCCCTTT TACTACCTGT TGGCTAATTT
251 AGCTGCTGCC GATTTCTTCG CTGGAATTGC CTATGTATTC CTGATGTTTA
301 ACACAGGCCC AGTTTCAAAA ACTTTGACTG TCAACCGCTG GTTTCTCCGT
351 CAGGGGCTTC TGGACAGTAG CTTGACTGCT TCCCTACCA ACTTGCTGGT
401 TATCGCCGTG GAGAGGCACA TGTCAATCAT GAGGATGCGG GTCCATAGCA
451 ACCTGACCAA AAAGAGGGTG AACTGCTCA TTTTGCTTGT CTGGGCCATC
501 GCCATTTTTA TGGGGGCGGT CCCCACTG GGCTGGAATT GCCTCTGCAA
551 CATCTCTGCC TGCTCTTCCC TGGCCCCCAT TTACAGCAGG AGTTACCTTG
601 TTTTCTGGAC AGTGTCCAAC CTCATGGCCT TCCTCATCAT GGTTGTGGTG
651 TACCTGCGGA TCTACGTGTA CGTCAAGAGG AAAACCAACG TCTTGCTCTC
701 GCATACAAGT GGGTCCATCA GCCGCCGAG GACACCCATG AAGCTAATGA
751 AGACGGTGAT GACTGTCTTA GGGGCGTTTG TGGTATGCTG GACCCCGGGC
801 CTGGTGTTTC TGCCCCCTCGA CGGCCTGAAC TGCAGGCAGT GTGGCGTGCA
851 GCATGTGAAA AGGTGGTTCC TGCTGCTGGC GCTGCTCAAC TCCGTCGTGA
901 ACCCCATCAT CTACTCCTAC AAGGACGAGG ACATGTATGG CACCATGAAG
951 AAGATGATCT GCTGCTTCTC TCAGGAGAAC CCAGAGAGGC GTCCCTCTCG
1001 CATCCCCCTC ACAGTCCTCA GCAGGAGTGA CACAGGCAGC CAGTACATAG
1051 AGGATAGTAT TAGCCAAGGT GCAGTCTGCA ATAAAAGCAC TTCCTAACT
1101 CTGGATGCCT CTYGGCCAC CCAGGCCTCC TCTGGGAAAA GAGCTGTAA
1151 GAATGATTAC CTGTCTCTAA CAAAGCCCAT GTACAGTGTT ATTTGAGGTC
1201 TCCATTAATC ACTGCTAGAT TTCTTTAAAA AATTTTTTTT CATAGTTTAA
1251 AAGCATGGGC AGTAAAGAGA GGACCTGCTG CATTTAGAGA AAGCACAGgt
1301 cgacgcggcc gcgaattcct ttgcttttta ccctggaaga aatactcgag
1351 catgcat

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Figure 3B: cDNA sequence of clone pC3-hEDG5#3.4 from the region encoding a hEDG5 polypeptide

1 ATGAATGAGT GTCACATATGA CAAGCACATG GACTTTTTTTT ATAATAGGAG
51 CAACACTGAT ACTGTCGATG ACTGGACTGG AACAAAGCTT GTGATTGTTT
101 TGTGTGTTGG GACGTTTTTC TGCCTGTTTA TTTTTTTTTT TAATTCTCTG
151 GTCATCGCGG CAGTGATCAA AAACAGAAAA TTTCATTTCC CCTTCTACTA
201 CCTGTTGGCT AATTGGGCTG CTGCCGATTT CTTCGCTGGA ATTGCCTATG
251 TATTCTGAT GTTTAACACA GGCCCAAGTTT CAAAACTTT GACTGTCAAC
301 CGCTGGTTTC TCCGTCAGGG GCTTCTGGAC AGTAGCTTGA CTGCTTCCCT
351 CACCAACTTG CTGGTTATCG CCGTGGAGAG GCACATGTCA ATCATGAGGA
401 TGCGGGTCCA TAGCAACCTG ACCAAAAAGA GGGTGACACT GCTCATTTTG
451 CTTGTCTGGG CCATCGCCAT TTTTATGGGG GCGGTCCCCA CACTGGGCTG
501 GAATTGCCTC TGCAACATCT CTGCCTGCTC TTCCCTGGCC CCCATTTACA
551 GCAGGAGTTA CCTTGTTTTT TGGACAGTGT CCAACCTCAT GGCCTTCCTC
601 ATCATGGTTG TGGGTACCT GCGGATCTAC GTGTACGTCA AGAGGAAAAC
651 CAACGTCTTG TCTCCGCATA CAAGTGGGTC CATCAGCCGC CGGAGGACAC
701 CCATGAAGCT AATGAAGACG GTAATGACTG TCTTAGGGGC GTTTGTGGTA
751 TGCTGGACCC CGGGCCTGGT GGTCTGCTC CTCGACGGCC TGAAGTGCAG
801 GCAGTGTGGC GTGCAGCATG TGAAAAGGTG GTTCCTGCTG CTGGCGCTGC
851 TCAACTCCGT CGTGAACCCT ATCATCTACT CCTACAAGGA CGAGGACATG
901 TATGGCACCA TGAAGAAGAT GATCTGCTGC TTCTCTCAGG AGAAGCCAGA
951 GAGGCGTCCC TCTCGCATCC CCTCCACAGT CCTCAGCAGG AGTGACACAG
1001 GCAGCCAGTA CATAGAGGAT AGTATTAGCC AAGGTGCAGT CTGCAATAAA
1051 AGCACTTCCT AA

Figure 3C: cDNA sequence of clone pC3-hEDG5#28 from the region encoding a hEDG5 polypeptide.

1 ATGAATGAGT GTCACATGA CAAGCACATG GACTTTTTTT ATAATAGGGG
51 CAACACTGAT ACTGTCGATG ACTGGACAGG AACAAAGCTT GTGATTGTTT
101 TGTGTGTtGG GACGTTTTTC TGCCTGTTTA TTTTTTTTTT TAATTCTCTG
151 GTCATCGCGG CAGTGATCAA AAACAGAAAA TTTCATTTCC CCTTCTACTA
201 CCTGTTGGCT AATTTAGCTG CTGCCGATTT CTTGCTGGA ATTGCCTATG
251 TATTCCTGAT GTTTAACACA GGCCCAAGTTT CAAAACTTT GACTGTCAAC
301 CGCTGGTTTC TCCGTCAGGG GCTTCTGGAC AGTAGCTTGA CTGCTTCCCT
351 CACCAACTTG CTGGTTATCG CCGTGGAGAG GCACATGTCA ATCATGAGGA
401 TGCGGGTCCA TAGCAACCTG ACCAAAAAGA GGGTGACACT GCTCATTTTG
451 CTTGTCTGGG CCATCGCCAT TTTTATGGGG GCGGTCCCCA CACTGGGctG
501 GAATTGCCTC TGCAAcATcT CTGCCTGcTC TTCCCTGGCC CCCATTTACA
551 GCAGGAGTTA CCTTGTTTTT TGGACAGTGT CcAACCTCAT GGCcTTcCTC
601 ATCATGGTTG TGGTGTACCT GCGGATcTAC GTGtACGTCA AGAGGAAAAC
651 CAAcGTCTTG TCTCCGCAtA CAAGTGGGTC CATCAGCCGC CGGAGGACAC
701 CCATGAAGCT AATGAAGACG GTGATGACTG TCTTAGGGGC GTTTGTGGTA
751 TGCTGGACCC CGGGCCTGGT GGTTCTGCTC CTCGACGGCC TGAActGCAG
801 GCAGTGTGGC GTGCAGCATG TGAAAAGGTG GTTCCTGCTG CTGGCGCTGC
851 TCAACTCCGT CGTGAACCCC ATCATCTACT CCTACAAGGA CGAGGACATG
901 TATGGCACCA TGAAGAAgAT GATCTGCTGC TTCTCTCAGG AGAACCAGGA
951 GAGGCGTCCC TCTCGCATCC CCTCCACAGT CCTCAGCAGG AGTGACACAG
1001 GCAGCCAGTA CATAGAGGAT AGTATTAGCC AAGGTGCAGT CTGCAATAAA
1051 AGCACTTCCT AA

SECRET

UNCLASSIFIED EIGHT (D.L. 24)

Figure 4A (cont.)

A S L T N L L V I A V E R H M S I M R M
CTGCTTCCCTCACCAACTTGCTGGTTATCGCCGTGGAGAGGCACATGTCAATCATGAGGA
601 -----+-----+-----+-----+-----+-----+-----+ 660
GACGAAGGGAGTGGTTGAACGACCAATAGCGGCACCTCTCCGTGTACAGTTAGTACTCCT

R V H S N L T K K R V T L L I L L V W A
TGCGGGTCCATAGCAACCTGACCAAAAAGGGTGACACTGCTCATTTTGCTTGTCTGGG
661 -----+-----+-----+-----+-----+-----+-----+ 720
ACGCCCAGGTATCGTTGGACTGGTTTTTCTCCCACTGTGACGAGTAAAACGAACAGACCC

I A I F M G A V P T L G W N C L C N I S
CCATCGCCATTTTATGGGGGCGGTCCCCACACTGGGCTGGAATTGCCTCTGCAACATCT
721 -----+-----+-----+-----+-----+-----+-----+ 780
GGTAGCGGTAAAAATACCCCCGCCAGGGGTGTGACCCGACCTTAACGGAGACGTTGTAGA

A C S S L A P I Y S R S Y L V F W T V S
CTGCCTGCTCTTCCCTGGCCCCCATTTACAGCAGGAGTTACCTTGTTTTCTGGACAGTGT
781 -----+-----+-----+-----+-----+-----+-----+ 840
GACGGACGAGAAGGGACCGGGGGTAAATGTCGTCCTCAATGGAACAAAAGACCTGTACA

N L M A F L I M V V V Y L R I Y V Y V K
CCAACCTCATGGCCTTCCTCATCATGGTTGTGGTGTACCTGCGGATCTACGTGTACGTCA
841 -----+-----+-----+-----+-----+-----+-----+ 900
GGTTGGAGTACCGGAAGGAGTAGTACCAACACCACATGGACGCCTAGATGCACATGCAGT

R K T N V L S P H T S G S I S R R R T P
AGAGGAAAACCAACGTCTTGTCTCCGCATACAAGTGGGTCCATCAGCCGCCGGAGGACAC
901 -----+-----+-----+-----+-----+-----+-----+ 960
TCTCCTTTTGGTTGCAGAACAGAGGCGTATGTTACCCAGGTAGTCGGCGGCCTCCTGTG

M K L M K T V M T V L G A F V V C W T P
CCATGAAGCTAATGAAGACGGTGATGACTGTCTTAGGGGCGTTTGTGGTATGCTGGACCC
961 -----+-----+-----+-----+-----+-----+-----+ 1020
GGTACTTCGATTACTTCTGCCACTACTGACAGAATCCCCGCAAACACCATAACGACCTGGG

G L V V L P L D G L N C R Q C G V Q H V
CGGGCCTGGTGGTTCTGCCCTCGACGGCCTGAAGTGCAGGCAGTGTGGCGTGCAGCATG
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
GCCCCGACCACCAAGACGGGGAGCTGCCGGACTTGACGTCCGTACACCCGCACGTCGTAC

K R W F L L L A L L N S V V N P I I Y S
TGAAAAGGTGGTTCTTGCTGCTGGCGCTGCTCAACTCCGTCTGTAACCCCATCATCTACT
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
ACTTTTCCACCAAGGACGACGACCGCGACGAGTTGAGGCAGCACTTGGGGTAGTAGATGA

Y K D E D M Y G T M K K M I C C F S Q E
CCTACAAGGACGAGGACATGTATGGCACCATGAAGAAGATGATCTGCTGCTTCTCTCAGG
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
GGATGTTCTGCTCCTGTACATACCGTGGTACTTCTTCTACTAGACGACGAAGAGAGTCC

N P E R R P S R I P S T V L S R S D T G
AGAACCCAGAGAGGCGTCCCTCTCGCATCCCCCTCCACAGTCCCTCAGCAGGAGTGACACAG
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
TCTTGGGTCTCTCCGCAGGGAGAGCGTAGGGGAGGTGTGAGGAGTCGTCTCTCACTGTGTC

S Q Y I E D S I S Q G A V C N K S T S *
GCAGCCAGTACATAGAGGATAGTATTAGCCAAGGTGCAGTCTGCAATAAAAGCACTTCCT
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
CGTCGGTCATGTATCTCCTATCATAATCGGTTCCACGTGACGAGTTATTTTCGTGAAGGA

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Figure 4A (cont.)

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1321  AAACTCTGGATGCCTCTYGGCCCACCCAGGCCTCCTCTGGGAAAAGAGCTGTTAAGAATG
-----+-----+-----+-----+-----+-----+-----+
TTTGAGACCTACGGAGARCCGGGTGGGTCCGGAGGAGACCCTTTTCTCGACAATTCTTAC
1380

1381  ATTACCTGTCTCTAACAAAGCCCATGTACAGTGTTATTTGAGGTCTCCATTAATCACTGC
-----+-----+-----+-----+-----+-----+-----+
TAATGGACAGAGATTGTTTCGGGTACATGTACACAATAAACTCCAGAGGTAATTAGTGACG
1440

1441  TAGATTTCTTTAAAAAATTTTTTTTCATAGTTTAAAGCATGGGCAGTAAAGAGAGGACC
-----+-----+-----+-----+-----+-----+-----+
ATCTAAAGAAATTTTTTAAAAAAAAGTATCAAATTTTCGTACCCGTCATTTCTCTCTCTGG
1500

1501  TGCTGCATTTAGAGAAAGCACAG
-----+-----+-----+-----+-----+-----+
ACGACGTAAATCTCTTTTCGTGTC
1523

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Figure 4B: Predicted amino acid sequence of hEDG5 encoded by clone pC3-hEDG5#3.4

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1  MNECHYDKHM DFFYNRSNTD TVDDWTGTKL VIVLCVGTFE CLFIFFSNL
51  VIAAVIKNRK FHFPFYLLA NLAAADFFAG IAYVFLMNT GPVSKTLTVN
101 RWFLRQGLLD SSLTASLTNL LVIAVERHMS IMRMRVHSNL TKKRVTLILL
151 LVWAIAIFMG AVPTLGWNCL CNISACSSLA PIYSRSLVF WTVSNLMAFL
201 IMVVVYLRIY VYVKRKTNL SPHTSGSISR RRTPMKLMKT VMTVLGAFVV
251 CWTPGLVLL LDGLNCRQCG VQHVCRWFL LALLNSVNP IIYSYKDEDM
301 YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK
351 STS

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Figure 4C: Predicted amino acid sequence of hEDG5 encoded by clone pC3-hEDG5#28.

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1  MNECHYDKHM DFFYNRGNTD TVDDWTGTKL VIVLCVGTFE CLFIFFSNL
51  VIAAVIKNRK FHFPFYLLA NLAAADFFAG IAYVFLMNT GPVSKTLTVN
101 RWFLRQGLLD SSLTASLTNL LVIAVERHMS IMRMRVHSNL TKKRVTLILL
151 LVWAIAIFMG AVPTLGWNCL CNISACSSLA PIYSRSLVF WTVSNLMAFL
201 IMVVVYLRIY VYVKRKTNL SPHTSGSISR RRTPMKLMKT VMTVLGAFVV
251 CWTPGLVLL LDGLNCRQCG VQHVCRWFL LALLNSVNP IIYSYKDEDM
301 YGTMKKMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK
351 STS

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Figure 5A: Alignment of predicted amino acid sequences of HEDG5 translation products of clones pC3-hEdg5#3.4, pC3-hEdg5-3 and pC3-hEdg5#28. Amino acid substitutions are indicated in reverse bold text.

	1				50
he5#3.4_981216	MNECHYDKHM	DDFYNRSNTD	TVDDWTGTKL	VIVLCVGTFF	CLFIFFSNL
hsedg5	MNECHYDKHM	DDFYNRSNTD	TVDDWTGTKL	VIVLCVGTFF	CLFIFFSNL
he5#28_981215	MNECHYDKHM	DDFYNR Q NTD	TVDDWTGTKL	VIVLCVGTFF	CLFIFFSNL
	51				100
he5#3.4_981216	VIAAVIKNRK	FHFPPYYLLA	NLAAADFFAG	IAYVFLMFNT	GPVSKTLTVN
hsedg5	VIAAVIKNRK	FHFPPYYLLA	NLAAADFFAG	IAYVFLMFNT	GPVSKTLTVN
he5#28_981215	VIAAVIKNRK	FHFPPYYLLA	NLAAADFFAG	IAYVFLMFNT	GPVSKTLTVN
	101				150
he5#3.4_981216	RWFLRQGLLD	SSLTASLTNL	LVIAVERHMS	IMRMRVHSNL	TKKRVTLIL
hsedg5	RWFLRQGLLD	SSLTASLTNL	LVIAVERHMS	IMRMRVHSNL	TKKRVTLIL
he5#28_981215	RWFLRQGLLD	SSLTASLTNL	LVIAVERHMS	IMRMRVHSNL	TKKRVTLIL
	151				200
he5#3.4_981216	LVWAIAIFMG	AVPTLGWNCL	CNISACSSLA	PIYSRSYLVF	WTVSNLMAFL
hsedg5	LVWAIAIFMG	AVPTLGWNCL	CNISACSSLA	PIYSRSYLVF	WTVSNLMAFL
he5#28_981215	LVWAIAIFMG	AVPTLGWNCL	CNISACSSLA	PIYSRSYLVF	WTVSNLMAFL
	201				250
he5#3.4_981216	IMVVVYLRIY	VYVKRKTNVL	SPHTSGSISR	RRTPMKLMKT	VMTVLGAFVV
hsedg5	IMVVVYLRIY	VYVKRKTNVL	SPHTSGSISR	RRTPMKLMKT	VMTVLGAFVV
he5#28_981215	IMVVVYLRIY	VYVKRKTNVL	SPHTSGSISR	RRTPMKLMKT	VMTVLGAFVV
	251				300
he5#3.4_981216	CWTPGLVVLL	LDGLNCRQCG	VQHVKRWFLL	LALLNSVVNP	IIYSYKDEDM
hsedg5	CWTPGLVVLL	LDGLNCRQCG	VQHVKRWFLL	LALLNSVVNP	IIYSYKDEDM
he5#28_981215	CWTPGLVVLL	LDGLNCRQCG	VQHVKRWFLL	LALLNSVVNP	IIYSYKDEDM
	301				350
he5#3.4_981216	YGTMKKMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK
hsedg5	YGTMKKMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK
he5#28_981215	YGTMKKMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK
	351				
he5#3.4_981216	STS-				
hsedg5	STS-				
he5#28_981215	STS-				

Figure 5B: Alignment of the amino acid sequence of the murine edg-5 with the amino acid sequence of the human edg-5 of the pC3-hEdg5-3.4 clone.

SCORES Init1: 1981 Initn: 2155 Opt: 2170 z-score: 384.5 E(): 2e-16
Smith-Waterman score: 2170; 91.2% identity in 354 aa overlap

	10	20	30	40	50	60
MEDG5	MNECHYDKRMDFFYNRSNTDTADEWTGKLVIVLCVGTFFCLFIFFSNSLVIAAVITNRK					
	: : : : :					
HEDG5-3.4	MNECHYDKHMDFFYNRSNTDTVDDWTGKLVIVLCVGTFFCLFIFFSNSLVIAAVIKNRK					
	10	20	30	40	50	60
	70	80	90	100	110	120
MEDG5	FHFPFYLLANLAAADFFAGIAYVFLMFNTGPVSKTLTVNRWFLRQGLDTSLTASLANL					
	: : : : :					
HEDG5-3.4	FHFPFYLLANLAAADFFAGIAYVFLMFNTGPVSKTLTVNRWFLRQGLDSSLTASLTNL					
	70	80	90	100	110	120
	130	140	150	160	170	180
MEDG5	LVIAVERHMSIMRMRVHSNLTKKRVTLILLVWAI AIFMGAVPTLGWNCLCNISACSSLA					
	: : : : :					
HEDG5-3.4	LVIAVERHMSIMRMRVHSNLTKKRVTLILLVWAI AIFMGAVPTLGWNCLCNISACSSLA					
	130	140	150	160	170	180
	190	200	210	220	230	240
MEDG5	PIYSRSYLIFWTVSNLLAFFIMVAVYVRIYMYVKRKTNVLSPHTSGSISRRRAPMKLMKT					
	: : : : :					
HEDG5-3.4	PIYSRSYLVFWTVSNLMAFLIMVVVYLRIYVYVKRKTNVLSPHTSGSISRRRTPMKLMKT					
	190	200	210	220	230	240
	250	260	270	280	290	300
MEDG5	VMTVLGAFVVCWTPGLVVLLDGLNCKQCNVQHVKRWFLLLALLNSVMNP IIYSYKDEDM					
	: : : : :					
HEDG5-3.4	VMTVLGAFVVCWTPGLVVLLDGLNCRQCGVQHVKRWFLLLALLNSVNP IIYSYKDEDM					
	250	260	270	280	290	300
	310	320	330	340	350	
MEDG5	YNTMRKMICCALQDSNTERRPSRNPSTIHSRSETGSQYLED SISQGPVCNKNGS					
	: :					
HEDG5-3.4	YGTMKKMICCFSQE-NPERRPSRIPSTVLSRSDTGSQYIED SISQGAVCNKSTS					
	310	320	330	340	350	

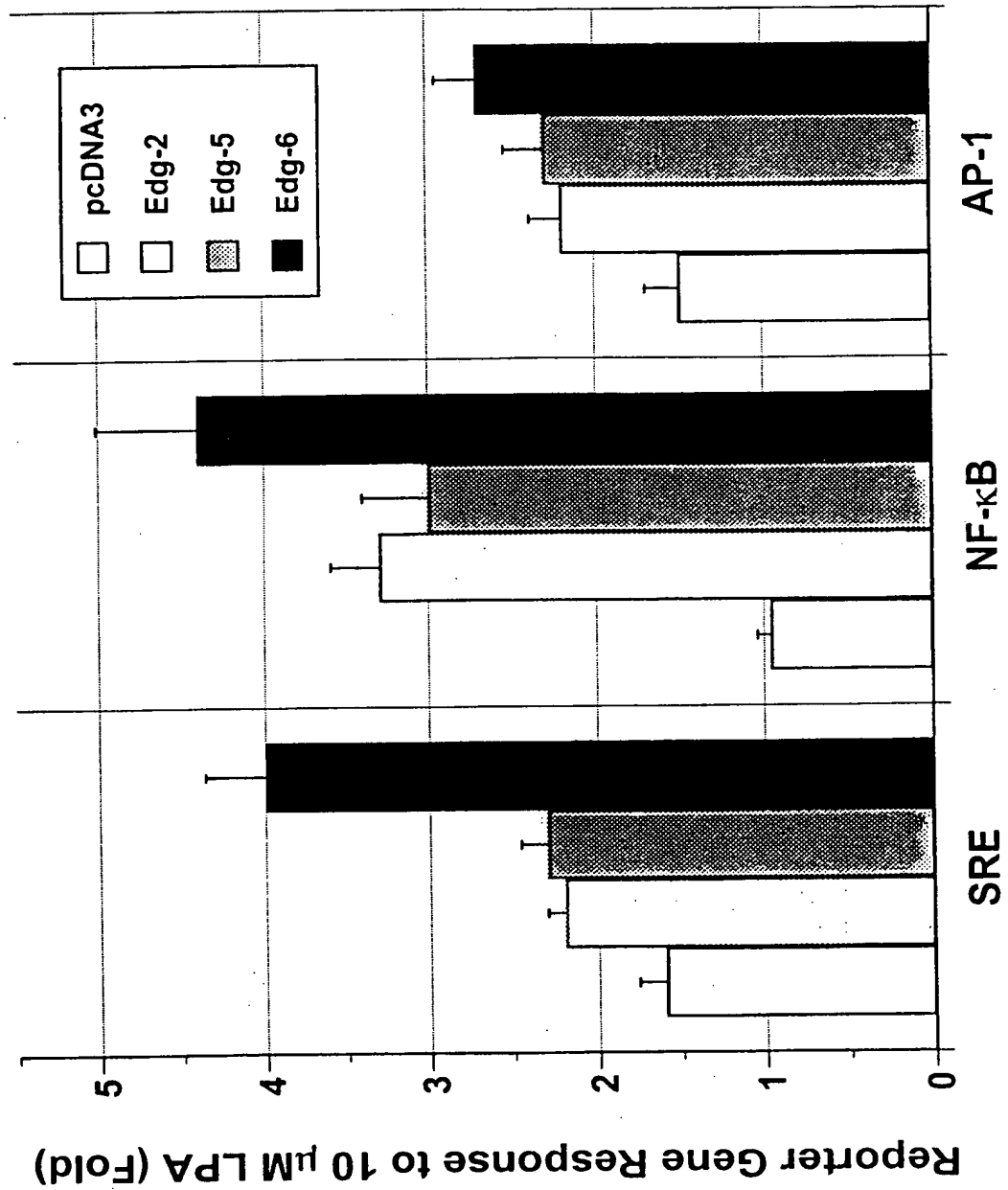


Figure 7